Figure 1

Spotted Filter

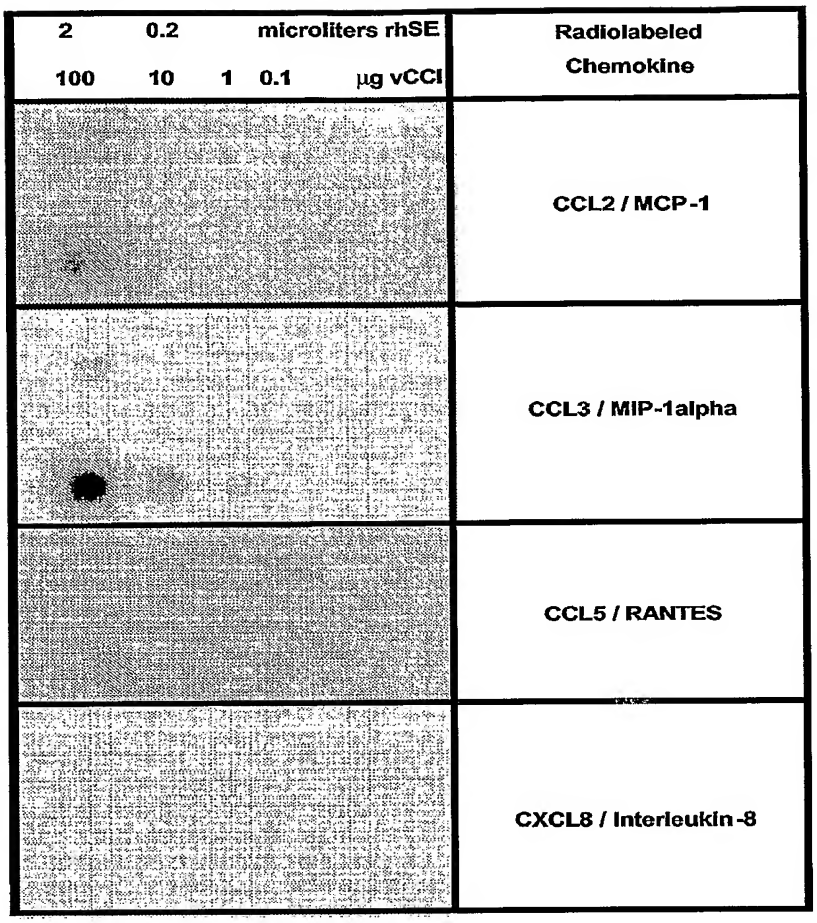


Figure 2

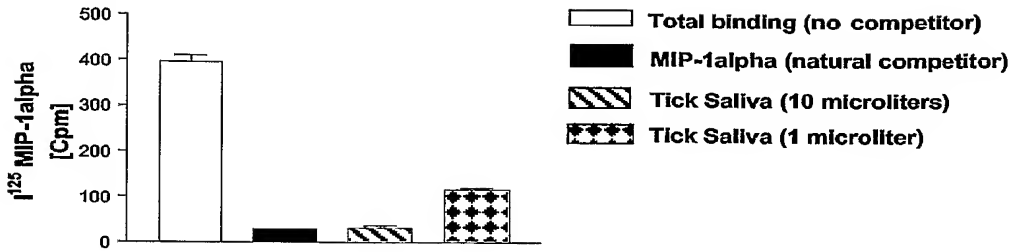
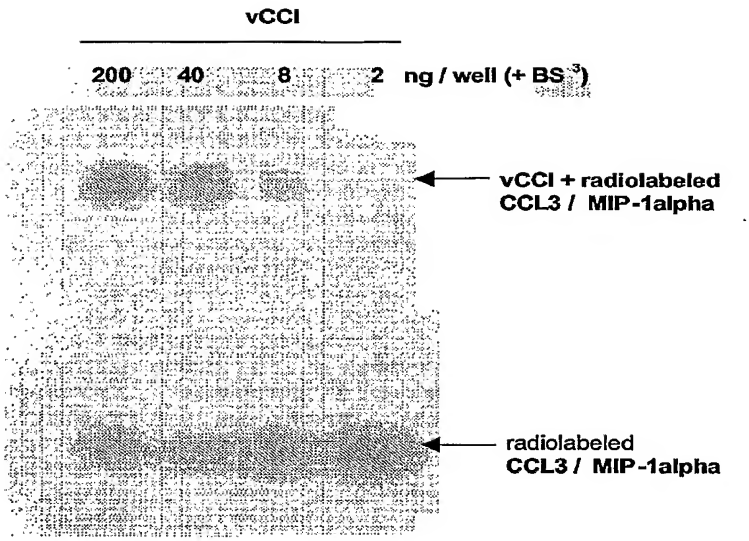

500
400
300
200
100
0
I^{125} MIP-1alpha [Cpm]
Total binding (no competitor)
MIP-1alpha (natural competitor)
Tick Saliva (10 microliters)
Tick Saliva (1 microliter)

Figure 3

A)


vCCI
200 40 8 2 ng / well (+ BS3)
vCCI + radiolabeled CCL3 / MIP-1alpha
radiolabeled CCL3 / MIP-1alpha

B)

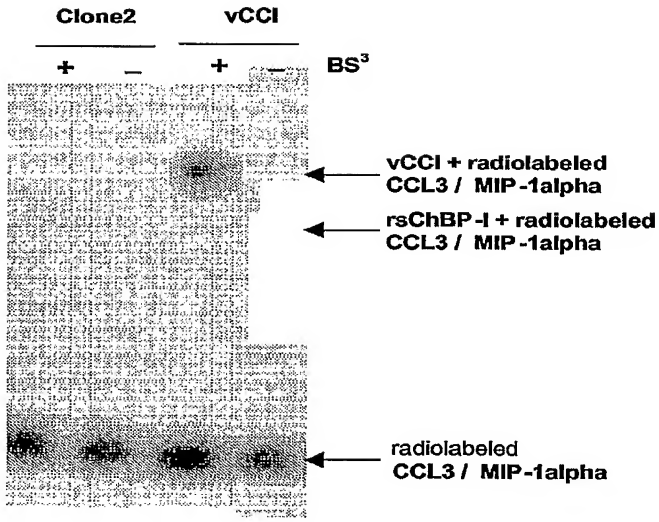

Clone2
vCCI
+ – + –
BS3
vCCI + radiolabeled CCL3 / MIP-1alpha
rsChBP-I + radiolabeled CCL3 / MIP-1alpha
radiolabeled CCL3 / MIP-1alpha

Figure 4

```
    1 GGCCATTACGGCCGGGGGTCCTTGCGCATTCGTGTAGAGCAGCAGCTCAAGTCTTCGAAG

   61 ATG CGC ACT TTC GGG GCT TCT CTT TTC GTT
    1 Met Arg Thr Phe Gly Ala Ser Leu Phe Val

   91 CTC CTC GCG ATT AGT GTC GCT TAC TGT GAC
   11 Leu Leu Ala Ile Ser Val Ala Tyr Cys Asp

  121 GTC CAA GAG CGC GGC CAT ACT TAC GTG ACC
   21 Val Gln Glu Arg Gly His Thr Tyr Val Thr

  151 AAA AAT GTG ACG GTC GAA AAC GGT GCC TGC
   31 Lys Asn Val Thr Val Glu Asn Gly Ala Cys

  181 GTG TTT GAA CGC AAC GTC ATT CCG GAT GGT
   41 Val Phe Glu Arg Asn Val Ile Pro Asp Gly

  210 GAA ACC AAA GCA CTG AAC AGC CCA TGC GTC
   51 Glu Thr Lys Ala Leu Asn Ser Pro Cys Val

  241 ATT TCC ACA TGC TAT GCA GCT GAC CGT AAA
   61 Ile Ser Thr Cys Tyr Ala Ala Asp Arg Lys

  271 GTG AAC TCG ACT CTC TGC CCG AAC TTC GGA
   71 Val Asn Ser Thr Leu Cys Pro Asn Phe Gly

  301 GTT GCG GAG GGC TGC CAT GTG GAG TGG ACC
   81 Val Ala Glu Gly Cys His Val Glu Trp Thr

  331 CCC GAT GGT GAA TAC CCG AAC TGC TGC CCG
   91 Pro Asp Gly Glu Tyr Pro Asn Cys Cys Pro

  361 AAG CAT GTG TGC CCT ACG GCC CCT GTT ACT
  101 Lys His Val Cys Pro Thr Ala Pro Val Thr

  391 TCT TAA TCGCATCACATCTGCGAAAATGAA
  111 Ser STOP

421 ACGTCGAGACATTCTTCTTTATGCCTTAAGAAATTAAACTGCAACGTCCGCAAAAATACA

481 TCCCCGCTTCAAATACGAACAAAATGCAGGATCAAATGCTATTAGGTTTCATGCTGAGTG

541 CAAGCTAAAATAAACAACTGAATCAGCGTTTAAAAAAAAAAAAAA
```

Figure 5

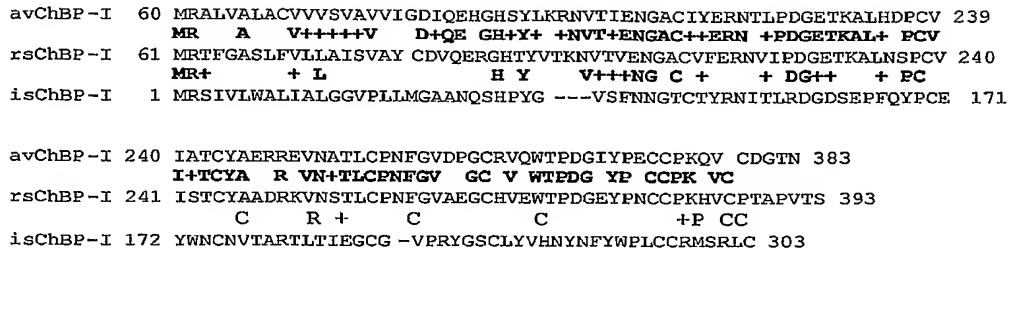

avChBP-I 60 MRALVALACVVVSVAVVIGDIQEHGHSYLKRNVTIENGACIYERNTLPDGETKALHDPCV 239
MR A V+++++V D+QE GH+Y+ +NVT+ENGAC++ERN +PDGETKAL+ PCV
rsChBP-I 61 MRTFGASLFVLLAISVAY CDVQERGHTYVTKNVTVENGACVFERNVIPDGETKALNSPCV 240
MR+ + L H Y V+++NG C + + DG++ + PC
isChBP-I 1 MRSIVLWALIALGGVPLLMGAANQSHPYG ---VSFNNGTCTYRNITLRDGDSEPFQYPCE 171
avChBP-I 240 IATCYAERREVNATLCPNFGVDPGCRVQWTPDGIYPECCPKQV CDGTN 383
I+TCYA R VN+TLCPNFGV GC V WTPDG YP CCPK VC
rsChBP-I 241 ISTCYAADRKVNSTLCPNFGVAEGCHVEWTPDGEYPNCCPKHVCPTAPVTS 393
C R + C C +P CC
isChBP-I 172 YWNCNVTARTLTIEGCG -VPRYGSCLYVHNYNFYWPLCCRMSRLC 303

Figure 6

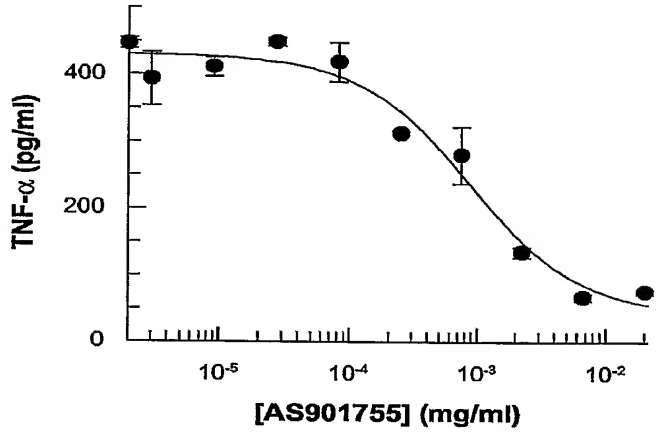
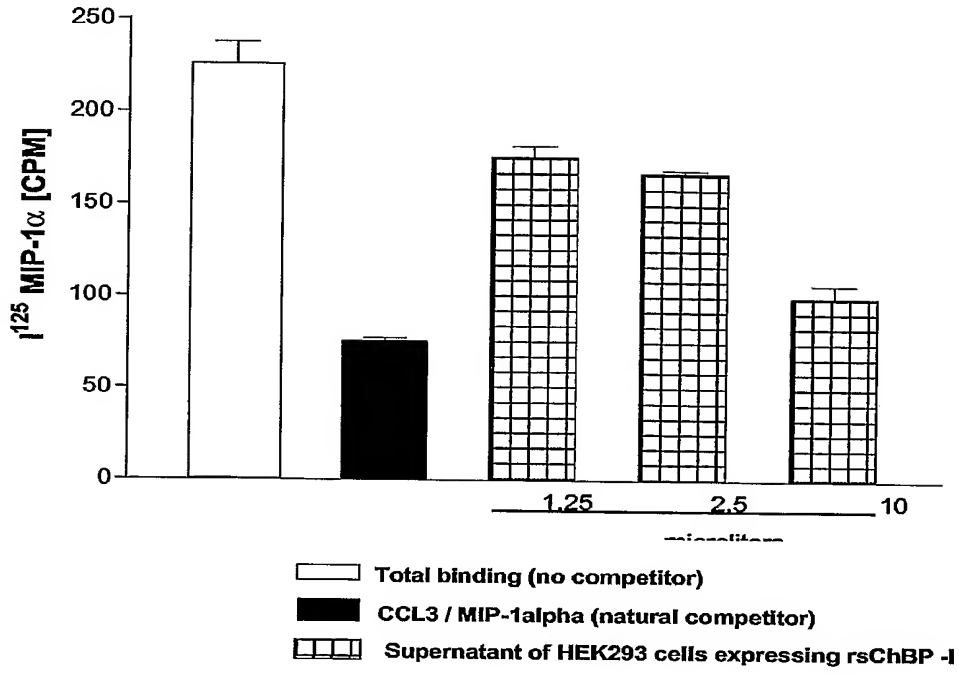


Figure 7


250
200
150
100
50
0
I^{125} MIP-1α [CPM]
1.25
2.5
10
Total binding (no competitor)
CCL3 / MIP-1alpha (natural competitor)
Supernatant of HEK293 cells expressing rsChBP -I